

FIG. 1A

Consensus Sequence

Symbol comparison table: blosum62.cmp CompCheck: 6430

Name: <u>hTRADEalpha_1</u>	Len: 423	Check: 4050	Weight: 1.00
Name: <u>hTRAIN_1</u>	Len: 423	Check: 4128	Weight: 1.00
Name: <u>hTRADEbeta_1</u>	Len: 423	Check: 7937	Weight: 1.00
Name: <u>hApo420pep</u>	Len: 423	Check: 8173	Weight: 1.00

//

hTRADEalpha_1	1	MALKVLLLEQE	KTFFTLVLL	GYLSCKVTCE	SGDCRQQEFR	DRSGNCVPCN	50
hTRAIN_1		MALKVLLLEQE	KTFFTLVLL	GYLSCKVTCE	SGDCRQQEFR	DRSGNCVPCN	
hTRADEbeta_1		MALKVLLLEQE	KTFFTLVLL	GYLSCKVTCE	TGDCRQQEFR	DRSGNCVPCN	
hApo420pep		MALKVLLLEQE	KTFFTLVLL	GYLSCKVTCE	SGDCRQQEFR	DRSGNCVPCN	
Consensus		MALKVLLLEQE	KTFFTLVLL	GYLSCKVTCE	SGDCRQQEFR	DRSGNCVPCN	
hTRADEalpha_1	51	QCGPGMELSK	ECGFGYGEDA	QCVTCRLHRF	KEDWGFQKCK	PCLDCAVVR	100
hTRAIN_1		QCGPGMELSK	ECGFGYGEDA	QCVTCRLHRF	KEDWGFQKCK	PCLDCAVVR	
hTRADEbeta_1		QCGPGMELSK	ECGFGYGEDA	QCVTCRLHRF	KEDWGFQKCK	PCLDCAVVR	
hApo420pep		QCGPGMELSK	ECGFGYGEDA	QCVTCRLHRF	KEDWGFQKCK	PCLDCAVVR	
Consensus		QCGPGMELSK	ECGFGYGEDA	QCVTCRLHRF	KEDWGFQKCK	PCLDCAVVR	
hTRADEalpha_1	101	FQKANCATS	DAICGDCPLG	FYRKTKLVGF	QDMECVPCGD	PPPPYEPHCA	150
hTRAIN_1		FQKANCATS	DAICGDCPLG	FYRKTKLVGF	QDMECVPCGD	PPPPYEPHCA	
hTRADEbeta_1		FQKANCATS	DAICGDCPLG	FYRKTKLVGF	QDMECVPCGD	PPPPYEPHCA	
hApo420pep		FQKANCATS	DAICGDCPLG	FYRKTKLVGF	QDMECVPCGD	PPPPYEPHCA	
Consensus		FQKANCATS	DAICGDCPLG	FYRKTKLVGF	QDMECVPCGD	PPPPYEPHCA	

FIG. 1B

hTRADEalpha_1	151	SKVNLVKIAS	TASSPRDTAL	AAVICSALAT	VLLALLILCV	IYCKRQFMEX	200
hTRAIN_1		SKVNLVKIAS	TASSPRDTAL	AAVICSALAT	VLLALLILCV	IYCKRQFMEX	
hTRADEbeta_1		SKVNLVKIAS	TASSPRDTAL	AAVICSALAT	VLLALLILCV	IYCKRQFMEX	
hApo420pep		SKVNLVKIAS	TASSPRDTAL	AAVICSALAT	VLLALLILCV	IYCKRQFMEX	
Consensus		SKVNLVKIAS	TASSPRDTAL	AAVICSALAT	VLLALLILCV	IYCKRQFMEX	
hTRADEalpha_1	201	KPSWSLRSQD	IQYNGSELSC	FDRPQLHEYA	HRACCQCRRD	SVQTCGPVRL	250
hTRAIN_1		KPSWSLRSQD	IQYNGSELSC	FDRPQLHEYA	HRACCQCRRD	SVQTCGPVRL	
hTRADEbeta_1		KPSWSLRSQD	IQYNGSELSC	LDRPQLHEYA	HRACCQCRRD	SVQTCGPVRL	
hApo420pep		KPSWSLRSQD	IQYNETELSC	FDRPQLHEYA	HRACCQCRRD	SVQTCGPVRL	
Consensus		KPSWSLRSQD	IQYNGSELSC	FDRPQLHEYA	HRACCQCRRD	SVQTCGPVRL	
hTRADEalpha_1	251	LPSMCCEEAC	SPNPATLGCG	VHSAASLQAR	NAGPAGEMVP	TFFGSLTQSI	300
hTRAIN_1		LPSMCCEEAC	SPNPATLGCG	VHSAASLQAR	NAGPAGEMVP	TFFGSLTQSI	
hTRADEbeta_1		LPSMCCEEAC	SPNPATLGCG	VHSAASLQAR	NAGPAGEMVP	TFFGSLTQSI	
hApo420pep		LPSMCCEEAC	SPNPATLGCG	VHSAASLQAR	NAGPAGEMVP	TFFGSLTQSI	
Consensus		LPSMCCEEAC	SPNPATLGCG	VHSAASLQAR	NAGPAGEMVP	TFFGSLTQSI	

FIG. 1C

hTRADEalpha_	301	CGEFSDAWPL	MQNPMSGDNI	SFCDSYPELT	GEDIHSLNPE	LESSTSLDSN	350
hTRAIN_1		CGEFSDAWPL	MQNPMSGDNI	SFCDSYPELT	GEDIHSLNPE	LESSTSLDSN	
hTRADEbeta_1		CGEFSDAWPL	MQNPMSGDNI	SFCDSYPELA	GEDIHSLNPE	LESSTSLDSN	
hApo420pep		CGEFSDAWPL	MQNPMSGDNI	SFCDSYPELT	GEDIHSLNPE	LESSTSLDSN	
Consensus		CGEFSDAWPL	MQNPMSGDNI	SPCDSYPELT	GEDIHSLNPE	LESSTSLDSN	
hTRADEalpha_	351	SSQDLVGGAV	PVQSHSEFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ	400
hTRAIN_1		SSQDLVGGAV	PVQSHSEFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ	
hTRADEbeta_1		SSQDLVGGAV	PVQSHSEFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ	
hApo420pep		SSQDLVGGAV	PVQSHSEFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ	
Consensus		SSQDLVGGAV	PVQSHSEFT	AATDLSRYNN	TLVESASTQD	ALTMRSQLDQ	
hTRADEalpha_	401	ESGAIHHPAT	QTSLQEA~~~	~~~			423
hTRAIN_1		ESGAVIHPAT	QTSLQEA~~~	~~~			
hTRADEbeta_1		ESGAIHHPAT	QTSLQVRQRL	GSL			
hApo420pep		ESGAVIHPAT	QTSLQVRQRL	GSL			
Consensus		ESGA-IHPAT	QTSLQ--QRL	GSL			

FIG. 2

TRADE- α	ESGAIHPATQTSLQEA		
TRADE- β	ESGAIHPATQTSLQVRQLGSL		
	401	416	423

FIG. 3

CRD1

NGFRp75	CPTGLYT.H	SGEC..CKAC	NLGEGVAQPC	..G.ANQTVC
OX40	CGDTYP..S	NDRC..CHEC	RPGNGMVSRC	..SRSQNTVCR
CD40	CREKQYL.L	NSQC..CSLC	QPGQKLVSDC	..TEFTETECL
TRADE	CRQQEFRDR	SGNCVPCNQC	GPGMELSKEC	GFGYGEDAQCV

CRD2

NGFRp75	PCLDSVTFS	DVVSATEPCK	PCTECVGLQS	MSAP...C	VE	ADDAVC
OX40	PC..GPGFY	NDVVSSKPCK	PCTWC.NLRS	GSEKQLCTA	TQDTVC	
CD40	PCGES.EFL	DTWNRETHCH	QHKYCDPNLG	LRVQOKGTSE	T.DTIC	
TRADE	TCRLHR.FK	EDWGFQK.CK	PCLDCAVVN.	.RFQKANCSA	TSDAIC	

FIG. 4

SEQ ID NO: 2 HUMAN	TRADE α	MALKVILEQEKTFETLLVLLGYSCKVTCE	CDR1	50
SEQ ID NO: 6 MOUSE	TRADE	MALKVILPHRTVLFAAILFLHLACKVSCET	CDR1	50
SEQ ID NO: 2 HUMAN	TRADE α	QCGPGMELSKCEGFGYGEDAQCVTCTRLH	CDR2	100
SEQ ID NO: 6 MOUSE	TRADE	QCGPGMELSKCEGFGYGEDAQCVPCTPRH	CDR2	100
SEQ ID NO: 2 HUMAN	TRADE α	FQKANCSTSDAICGDCPLPGFYRKTKLVGFQ	CDR2	150
SEQ ID NO: 6 MOUSE	TRADE	FQKANCSTSDAVCGDCPLPGFYRKTKLVGFQ	CDR2	150
SEQ ID NO: 2 HUMAN	TRADE α	SKVNLVKIISTASSPRDTALAAVICSALATV	CDR2	200
SEQ ID NO: 6 MOUSE	TRADE	SKVNLVKIISTASSPRDTALAAVICSALATV	CDR2	200
SEQ ID NO: 2 HUMAN	TRADE α	KPSWSLRSQDIQYNGSELSCFDRLPQLHE	CDR2	250
SEQ ID NO: 6 MOUSE	TRADE	KPSWSLRSQDIQYNGSELSCFDRLPQLHE	CDR2	250
SEQ ID NO: 2 HUMAN	TRADE α	IPSMCCEEACSPNPATLGCCHVHSAASLQ	CDR2	300
SEQ ID NO: 6 MOUSE	TRADE	IPSLCCEEARSARAVLGCGLRSPTTLQER	CDR2	300
SEQ ID NO: 2 HUMAN	TRADE α	CGEFSDAWPLMQNPVGGDNISFCDSYPE	CDR2	350
SEQ ID NO: 6 MOUSE	TRADE	CAEFSDAWPLMQNPVGGDS-SLCDSYPE	CDR2	349
SEQ ID NO: 2 HUMAN	TRADE α	SSQDLVGGAVPVQSHSENFTAAATDL	CDR2	400
SEQ ID NO: 6 MOUSE	TRADE	GGQDLVAGTALESNGVNSESTSPRHG	CDR2	399
SEQ ID NO: 2 HUMAN	TRADE α	ESGAVITHPATQTSLOFA	CDR2	417
SEQ ID NO: 6 MOUSE	TRADE	EDRENLTAMPTAFQDA	CDR2	416

FIG. 5A

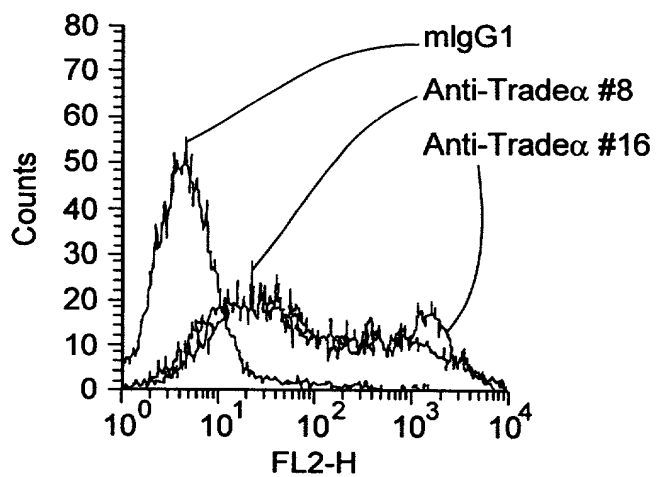


FIG. 5B

mAb # 8

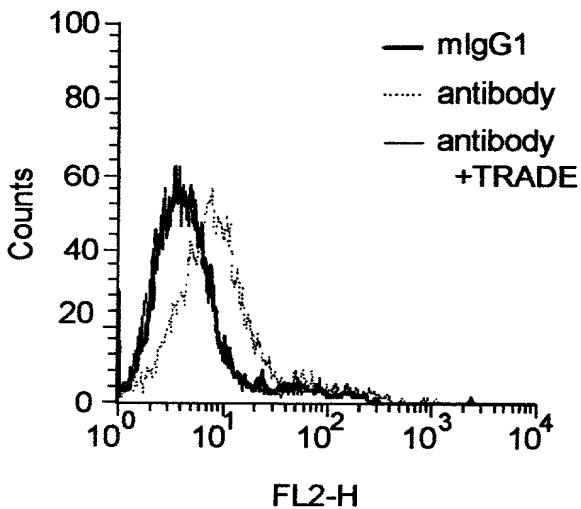


FIG. 5C

mAb#16

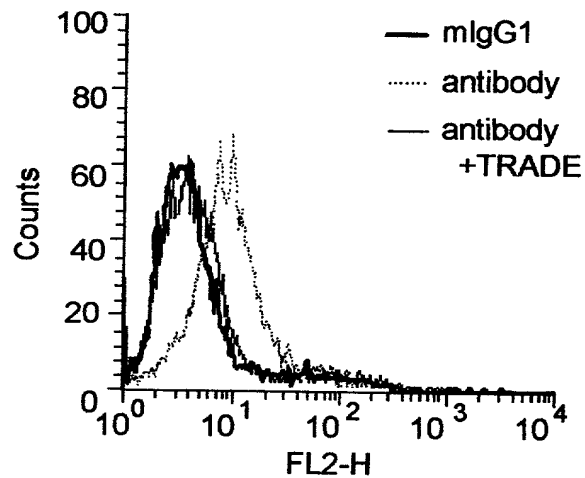


FIG. 6A

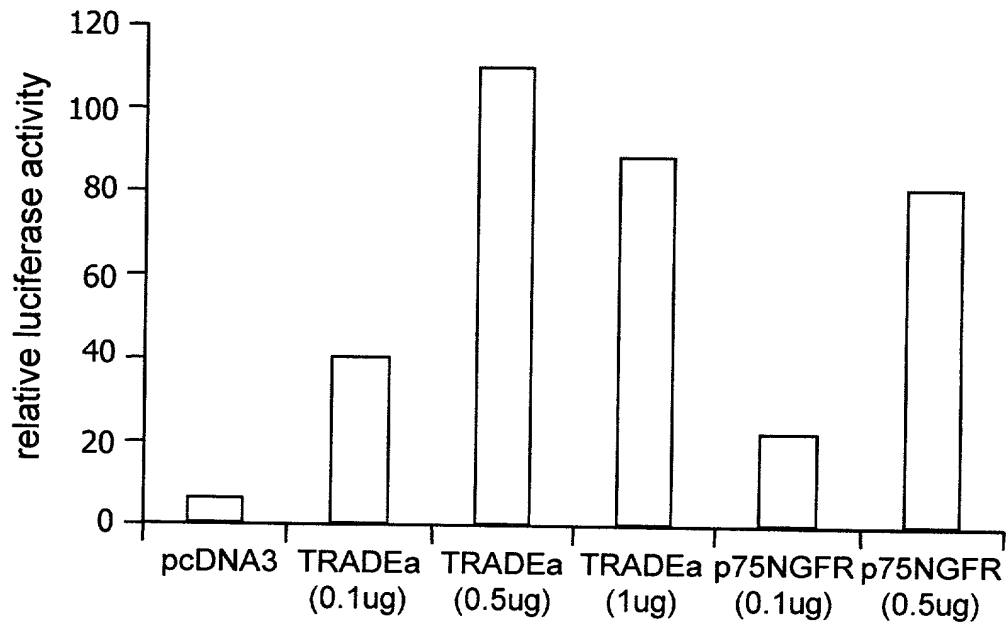


FIG. 6B

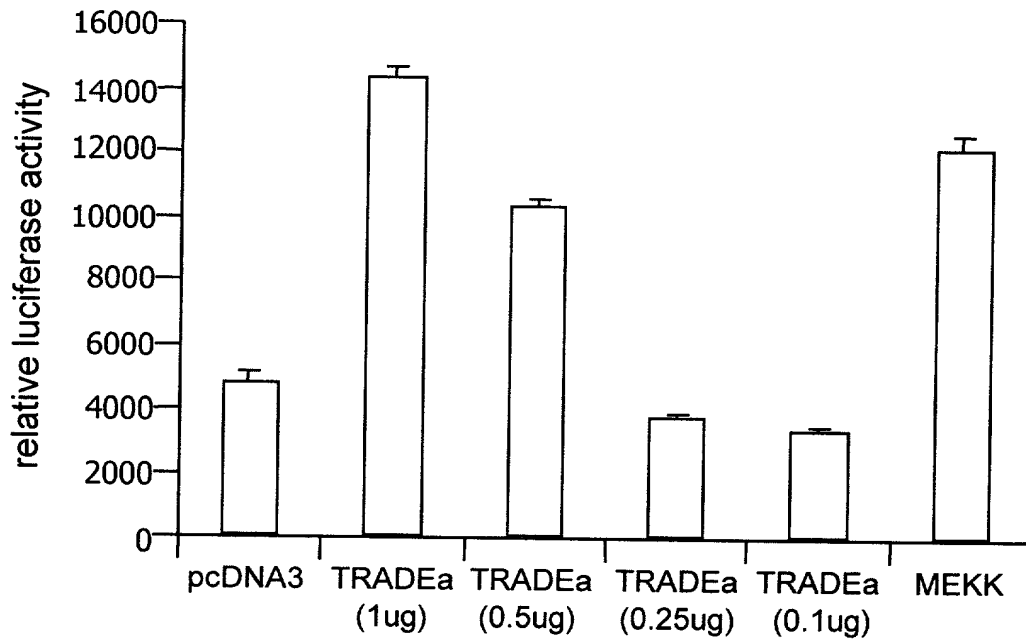


FIG. 7A

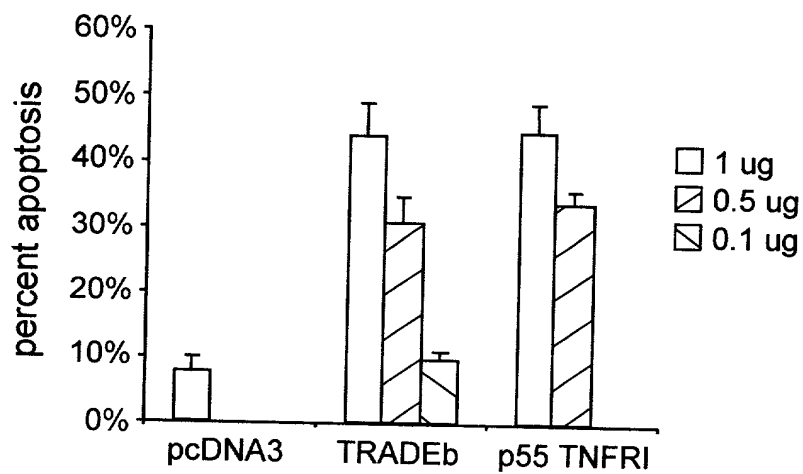


FIG. 7B

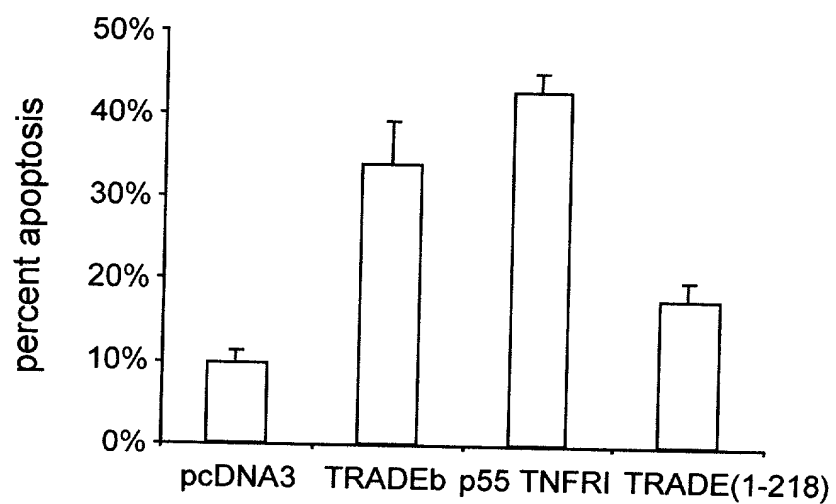


FIG. 8

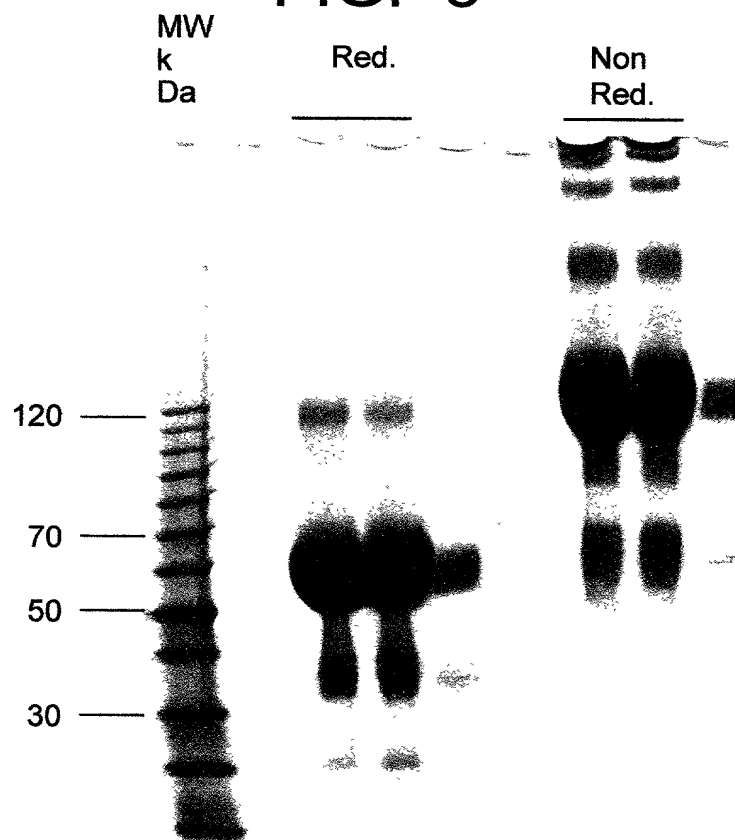
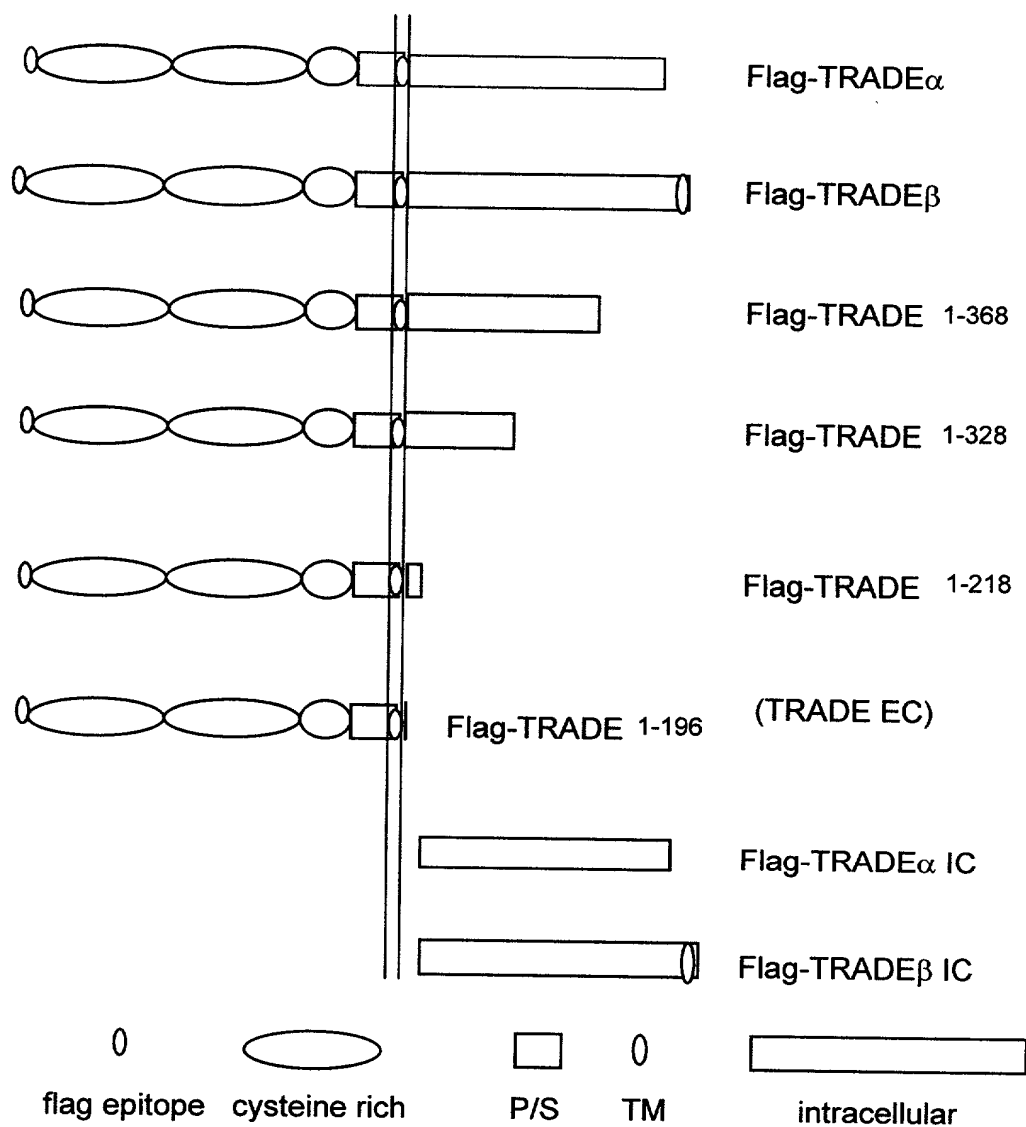


FIG. 9



Deletion analysis

FIG. 10

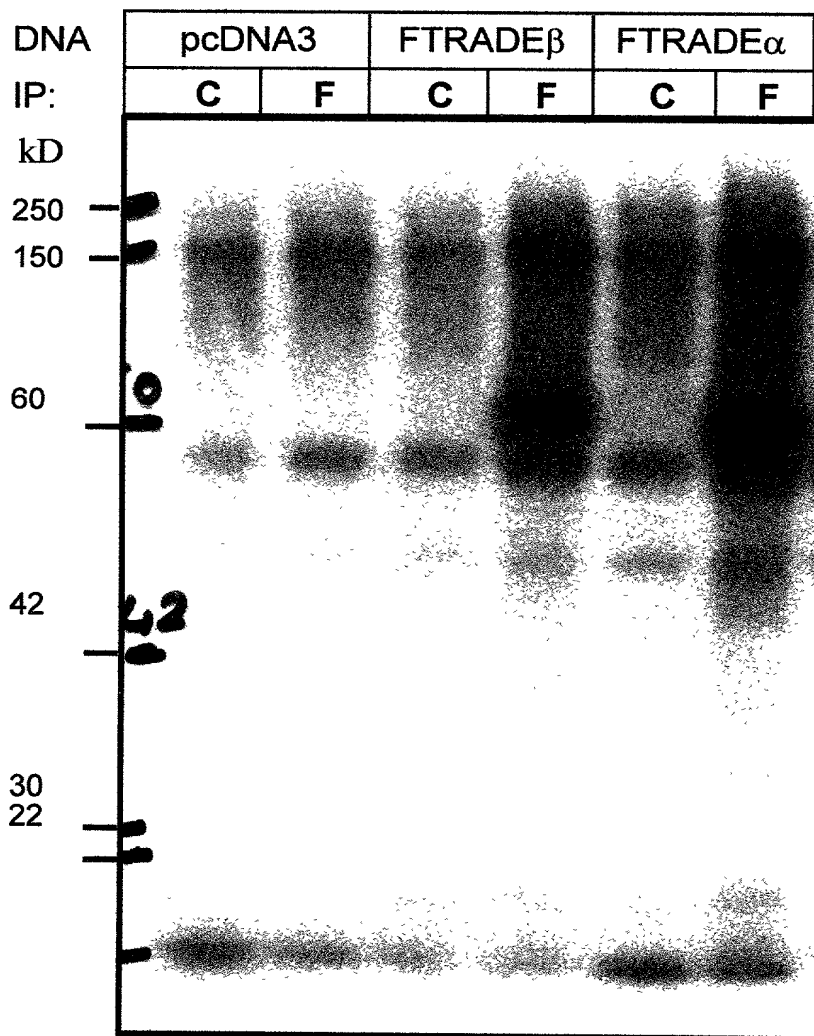
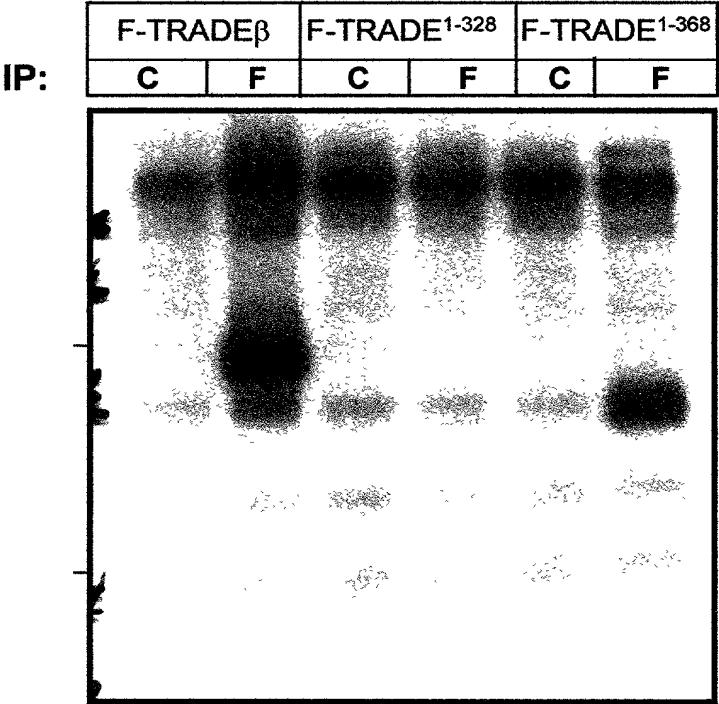
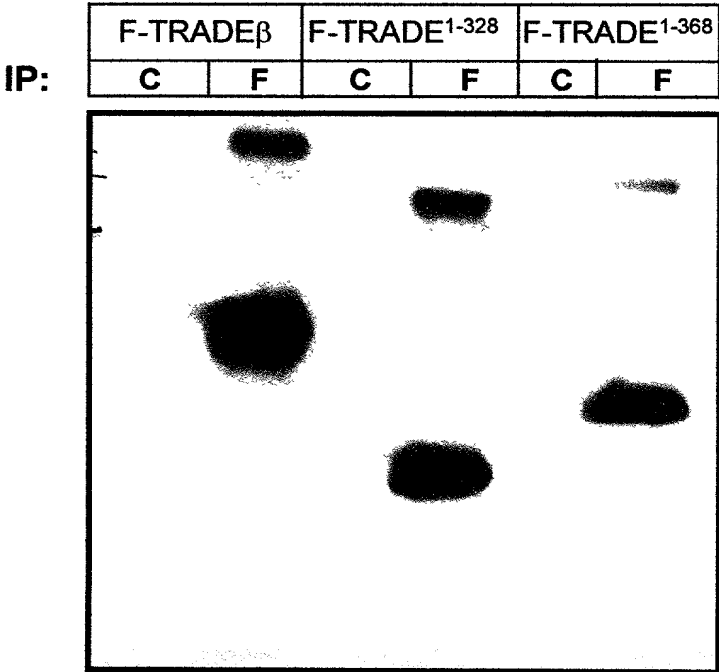


FIG. 11A



Kinase assay

FIG. 11B



anti-Flag blot

FIG. 12A

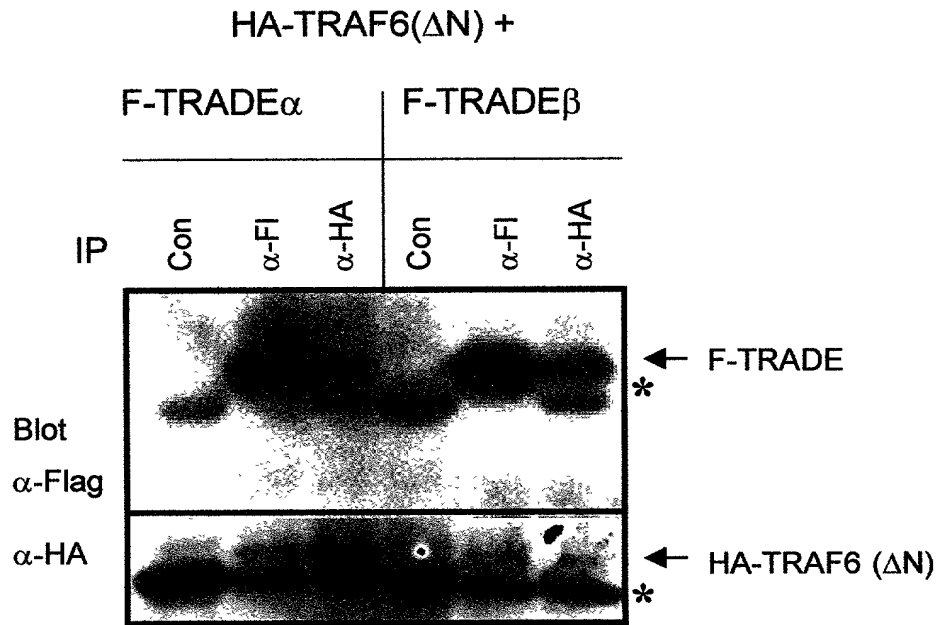


FIG. 12B

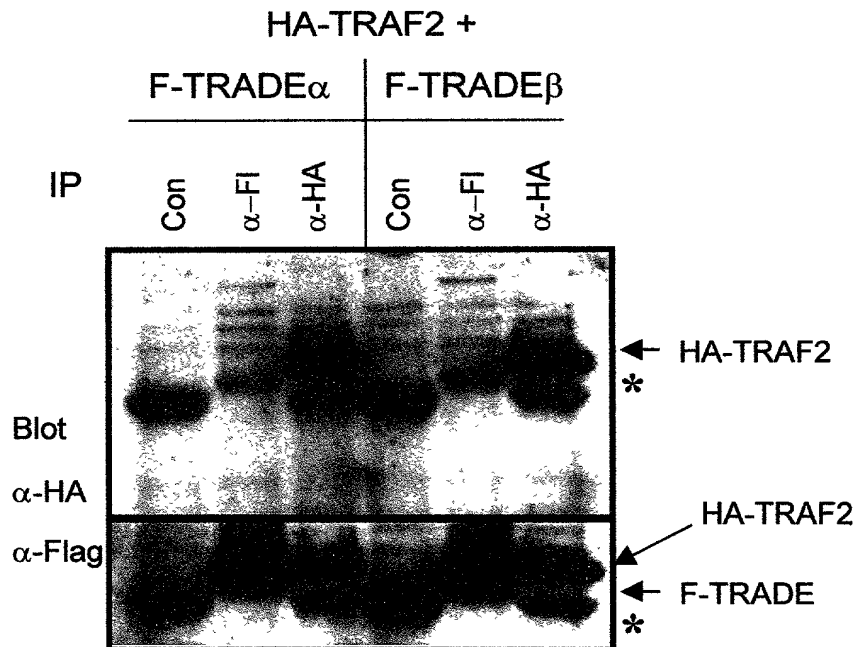


FIG. 13

HA-TRAF3+

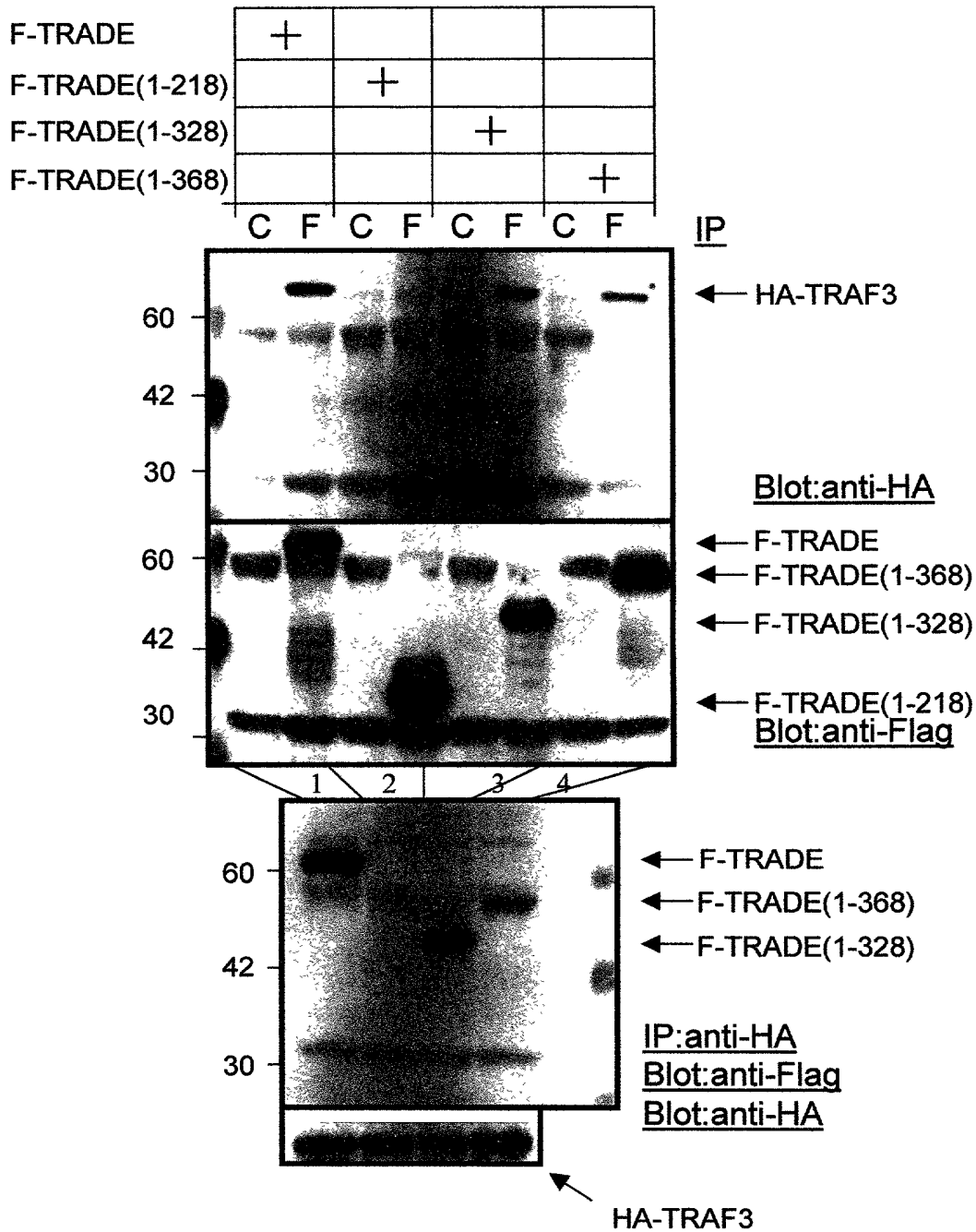


FIG. 14A

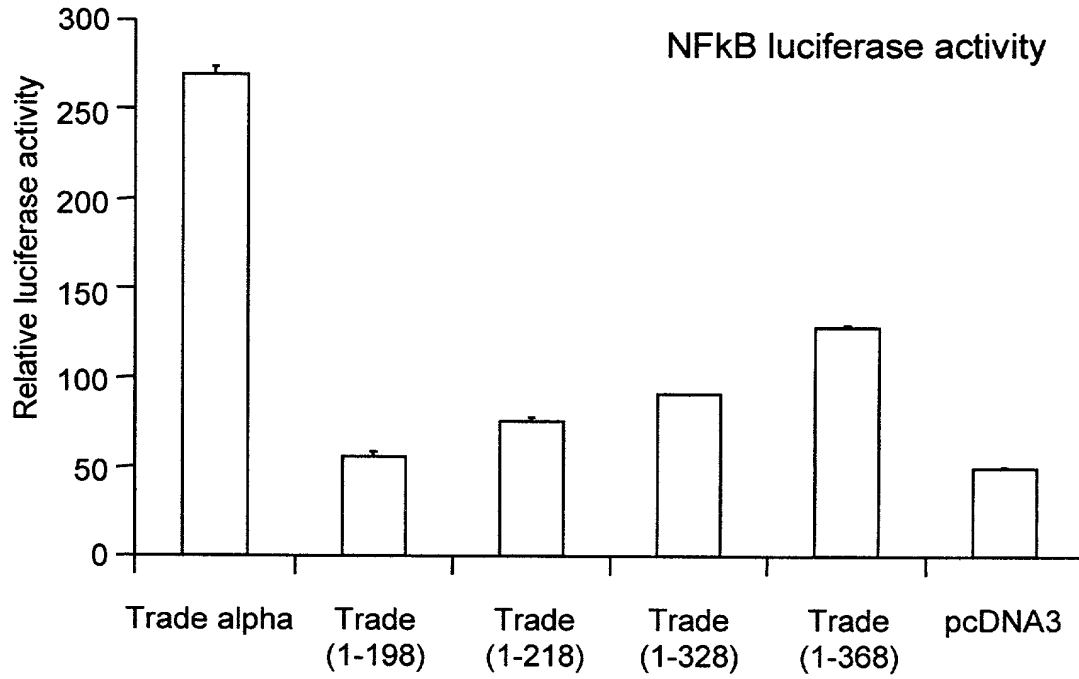


FIG. 14B

